

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: US 10,045,063 A

Source: TFW16

Date Processed by STIC: 7-29-04

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IFW16

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/045,063A

DATE: 11/29/2004
 TIME: 10:51:21

Input Set : A:\021123-0284981.ST25.txt
 Output Set: N:\CRF4\11292004\J045063A.raw

3 <110> APPLICANT: ALTENBUCHNER, Josef
 4 MATTES, Ralf
 5 PIETZSCH, Markus
 6 SYLDATK, Christoph
 7 WIESE, Anja
 8 WILMS, Burkard
 10 <120> TITLE OF INVENTION: RECOMBINANT L-N-CARBAMOYLASE FROM ARTHROBACTER AURESCENS AND
 11 METHOD OF PRODUCING L-AMINO ACIDS THEREWITH
 13 <130> FILE REFERENCE: 021123-0284981
 15 <140> CURRENT APPLICATION NUMBER: US 10/045063A
 16 <141> CURRENT FILING DATE: 2002-01-15
 18 <150> PRIOR APPLICATION NUMBER: US 09/285055
 19 <151> PRIOR FILING DATE: 1999-04-02
 21 <150> PRIOR APPLICATION NUMBER: DE 198 14 813.5
 22 <151> PRIOR FILING DATE: 1998-04-02
 24 <160> NUMBER OF SEQ ID NOS: 5
 26 <170> SOFTWARE: PatentIn version 3.3
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 1239
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Arthrobacter aurescens
 33 <400> SEQUENCE: 1
 34 gtgaccctgc agaaagcgca agcggcgccgca attgagaaag agatccggga gctctccgg 60
 36 ttctcggcag aaggccccgg tggttacccgg ctgacctaca ctccagagca tgccgcccgcg 120
 38 cggaaacacgc tcattgcggc tatgaaagcg gccgcctgta gcgttcgtga agacgcactc 180
 40 gaaacatca tcggccgacg tgaaggcact gatccggagc ttccctgcgt cgcggcgt 240
 42 tcacacttcg attctgtccg aaacggcgaa atgtttgatg gcactgcagg cgtggtgtgc 300
 44 gcccttgagg ctgccccgggt gatgtggag aacggctacg tgaatggca tccatttttag 360
 46 ttcatcgca tcgtggagga ggaaggggcc cgcttcagca gtggcatgtt gggggccgg 420
 48 gccattgcag gggttggtcgc cgacagggaa ctggactctt tgggtttagtga ggatggatg 480
 50 tccgttaggc agggcgctac tgccttcggc ttgaagccgg qcgaactgca qgctgcagcc 540
 52 cgctccggcg cgacactgcg tgcttttatac gaactacaca ttgaacaagg accgatcc 600
 54 gagcaggagc aaatagagat cggaggatgt aacctccatcg ttggcgatcg cgcattgcgg 660
 56 gttgccgtca aaggcagaag cgaccacgcg ggcacaaccc ccatgcaccc ggcggcaggat 720
 58 ggcgtgtac ccggcgctct catggtgagg gaggtcaacc gttcgatccaa cgatgcgg 780
 60 gatggcagac gttgtaccgt tggccaccc acagtggccc cgggtggagg caaccaggatc 840
 62 ccgggggagg tggacttcac actggacccg cgttctccgc atgaggagtc gtcggcggt 900
 64 ctgatcgacc gcatctcggt catggtcggc gaggtcgcccccaggccgg tgggtgtcc 960
 66 gatgtggatg aatttttcaa tctcagcccg gtgcagctgg ctccatgat ggtggacgcc 1020
 68 gttcgcaag cggcctcgcc tttcgatcc acacaccggg atatcagcag tggggccggc 1080
 70 cacgactcga tggatcgcc ccaggatcg gacgtcgaa tggtttcgt tccaaggccgt 1140
 72 gctggccgga gccacgttcc cgaagaatgg accgattcg atgacatcg caaaggaaact 1200
 74 gaggttgcgtcc tccggtaat gaaggactt gaccggtaaa 1239

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77 <210> SEQ ID NO: 2
 78 <211> LENGTH: 412
 79 <212> TYPE: PRT
 80 <213> ORGANISM: Arthrobacter aurescens
 82 <400> SEQUENCE: 2

84 Met Thr Leu Gln Lys Ala Gln Ala Ala Arg Ile Glu Lys Glu Ile Arg
 85 1 5 10 15
 88 Glu Leu Ser Arg Phe Ser Ala Glu Gly Pro Gly Val Thr Arg Leu Thr
 89 20 25 30
 92 Tyr Thr Pro Glu His Ala Ala Ala Arg Glu Thr Leu Ile Ala Ala Met
 93 35 40 45
 96 Lys Ala Ala Ala Leu Ser Val Arg Glu Asp Ala Leu Gly Asn Ile Ile
 97 50 55 60
 100 Gly Arg Arg Glu Gly Thr Asp Pro Glu Leu Pro Ala Ile Ala Val Gly
 101 65 70 75 80
 104 Ser His Phe Asp Ser Val Arg Asn Gly Gly Met Phe Asp Gly Thr Ala
 105 85 90 95
 108 Gly Val Val Cys Ala Leu Glu Ala Ala Arg Val Met Leu Glu Asn Gly
 109 100 105 110
 112 Tyr Val Asn Arg His Pro Phe Glu Phe Ile Ala Ile Val Glu Glu Glu
 113 115 120 125
 116 Gly Ala Arg Phe Ser Ser Gly Met Leu Gly Gly Arg Ala Ile Ala Gly
 117 130 135 140
 120 Leu Val Ala Asp Arg Glu Leu Asp Ser Leu Val Asp Glu Asp Gly Val
 121 145 150 155 160
 124 Ser Val Arg Gln Ala Ala Thr Ala Phe Gly Leu Lys Pro Gly Glu Leu
 125 165 170 175
 128 Gln Ala Ala Ala Arg Ser Ala Ala Asp Leu Arg Ala Phe Ile Glu Leu
 129 180 185 190
 132 His Ile Glu Gln Gly Pro Ile Leu Glu Gln Ile Glu Ile Gly
 133 195 200 205
 136 Val Val Thr Ser Ile Val Gly Val Arg Ala Leu Arg Val Ala Val Lys
 137 210 215 220
 140 Gly Arg Ser Asp His Ala Gly Thr Thr Pro Met His Leu Arg Gln Asp
 141 225 230 235 240
 144 Ala Leu Val Pro Ala Ala Leu Met Val Arg Glu Val Asn Arg Phe Val
 145 245 250 255
 148 Asn Glu Ile Ala Asp Gly Thr Val Ala Thr Val Gly His Leu Thr Val
 149 260 265 270
 152 Ala Pro Gly Gly Gly Asn Gln Val Pro Gly Glu Val Asp Phe Thr Leu
 153 275 280 285
 156 Asp Leu Arg Ser Pro His Glu Glu Ser Leu Arg Val Leu Ile Asp Arg
 157 290 295 300
 160 Ile Ser Val Met Val Gly Glu Val Ala Ser Gln Ala Gly Val Ala Ala
 161 305 310 315 320
 164 Asp Val Asp Glu Phe Phe Asn Leu Ser Pro Val Gln Leu Ala Pro Thr
 165 325 330 335
 168 Met Val Asp Ala Val Arg Glu Ala Ala Ser Ala Leu Gln Phe Thr His
 169 340 345 350

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172 Arg Asp Ile Ser Ser Gly Ala Gly His Asp Ser Met Phe Ile Ala Gln
173 355 360 365
176 Val Thr Asp Val Gly Met Val Phe Val Pro Ser Arg Ala Gly Arg Ser
177 370 375 380
180 His Val Pro Glu Glu Trp Thr Asp Phe Asp Asp Leu Arg Lys Gly Thr
181 385 390 395 400
184 Glu Val Val Leu Arg Val Met Lys Ala Leu Asp Arg
185 405 410
188 <210> SEQ ID NO: 3
189 <211> LENGTH: 17
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Radioactively marked oligonucleotide
197 <220> FEATURE:
198 <221> NAME/KEY: misc_feature
199 <222> LOCATION: (12)..(12)
200 <223> OTHER INFORMATION: n is A, G, C or T
202 <400> SEQUENCE: 3
--> 203 atgttygayg tnathgt 17
206 <210> SEQ ID NO: 4
207 <211> LENGTH: 30
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Primer
214 <400> SEQUENCE: 4
215 agaacatatg tttgacgtaa tagttaagaa 30
218 <210> SEQ ID NO: 5
219 <211> LENGTH: 28
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Primer
226 <400> SEQUENCE: 5
227 aaaaggatcc tcacttcgac gcctcgta 28

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 12

VERIFICATION SUMMARY

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L: 203 M: 341 W: (46) "n" or "Xaa" used, for SEQ ID#: 3 after pos.: 0